

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/525,535
Source: IFW16
Date Processed by STIC: 03/08/2007

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 03/08/2007

PATENT APPLICATION: US/10/525,535

TIME: 14:57:10

Input Set : N:\efs\03_08_07\10525535_efs\324503SequenceListing.txt

Output Set: N:\CRF4\03082007\J525535.raw

```

4 <110> APPLICANT: Wong, Justin
5      Winter, Jill
6      Lalehzadeh, Guita
7      Warne, Robert
9 <120> TITLE OF INVENTION: Compositions and Methods of Therapy for
10     Cancers Characterized by Expression of the Tumor-Associated
11     Antigen MN/CA IX
13 <130> FILE REFERENCE: PP019155.0004
15 <140> CURRENT APPLICATION NUMBER: US 10/525,535
16 <141> CURRENT FILING DATE: 2005-02-23
18 <150> PRIOR APPLICATION NUMBER: PCT/US2003/026612
19 <151> PRIOR FILING DATE: 2003-08-25
21 <150> PRIOR APPLICATION NUMBER: 60/405,577
22 <151> PRIOR FILING DATE: 2002-08-23
24 <160> NUMBER OF SEQ ID NOS: 10
26 <170> SOFTWARE: FastSEQ for Windows Version 4.0
28 <210> SEQ ID NO: 1
29 <211> LENGTH: 1380
30 <212> TYPE: DNA
31 <213> ORGANISM: Homo sapiens
33 <220> FEATURE:
34 <221> NAME/KEY: CDS
35 <222> LOCATION: (1)...(1380)
37 <400> SEQUENCE: 1
38 atg gct ccc ctg tgc ccc agc ccc tgg ctc cct ctg ttg atc ccg gcc      48
39 Met Ala Pro Leu Cys Pro Ser Pro Trp Leu Pro Leu Leu Ile Pro Ala
40 1          5          10          15
42 cct gct cca ggc ctc act gtg caa ctg ctg ctg tca ctg ctg ctt ctg      96
43 Pro Ala Pro Gly Leu Thr Val Gln Leu Leu Leu Ser Leu Leu Leu Leu
44          20          25          30
46 atg cct gtc cat ccc cag agg ttg ccc cgg atg cag gag gat tcc ccc      144
47 Met Pro Val His Pro Gln Arg Leu Pro Arg Met Gln Glu Asp Ser Pro
48          35          40          45
50 ttg gga gga ggc tct tct ggg gaa gat gac cca ctg ggc gag gag gat      192
51 Leu Gly Gly Gly Ser Ser Gly Glu Asp Asp Pro Leu Gly Glu Glu Asp
52          50          55          60
54 ctg ccc agt gaa gag gat tca ccc aga gag gag gat cca ccc gga gag      240
55 Leu Pro Ser Glu Glu Asp Ser Pro Arg Glu Glu Asp Pro Pro Gly Glu
56 65          70          75          80
58 gag gat cta cct gga gag gag gat cta cct gga gag gag gat cta cct      288
59 Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro
60          85          90          95
62 gaa gtt aag cct aaa tca gaa gaa gag ggc tcc ctg aag tta gag gat      336

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```

63 Glu Val Lys Pro Lys Ser Glu Glu Glu Gly Ser Leu Lys Leu Glu Asp
64      100      105      110
66 cta cct act gtt gag gct cct gga gat cct caa gaa ccc cag aat aat 384
67 Leu Pro Thr Val Glu Ala Pro Gly Asp Pro Gln Glu Pro Gln Asn Asn
68      115      120      125
70 gcc cac agg gac aaa gaa ggg gat gac cag agt cat tgg cgc tat gga 432
71 Ala His Arg Asp Lys Glu Gly Asp Asp Gln Ser His Trp Arg Tyr Gly
72      130      135      140
74 ggc gac ccg ccc tgg ccc cgg gtg tcc cca gcc tgc gcg ggc cgc ttc 480
75 Gly Asp Pro Pro Trp Pro Arg Val Ser Pro Ala Cys Ala Gly Arg Phe
76 145      150      155      160
78 cag tcc ccg gtg gat atc cgc ccc cag ctc gcc gcc ttc tgc ccg gcc 528
79 Gln Ser Pro Val Asp Ile Arg Pro Gln Leu Ala Ala Phe Cys Pro Ala
80      165      170      175
82 ctg cgc ccc ctg gaa ctc ctg ggc ttc cag ctc ccg ccg ctc cca gaa 576
83 Leu Arg Pro Leu Glu Leu Leu Gly Phe Gln Leu Pro Pro Leu Pro Glu
84      180      185      190
86 ctg cgc ctg cgc aac aat ggc cac agt gtg caa ctg acc ctg cct cct 624
87 Leu Arg Leu Arg Asn Asn Gly His Ser Val Gln Leu Thr Leu Pro Pro
88      195      200      205
90 ggg cta gag atg gct ctg ggt ccc ggg cgg gag tac cgg gct ctg cag 672
91 Gly Leu Glu Met Ala Leu Gly Pro Gly Arg Glu Tyr Arg Ala Leu Gln
92      210      215      220
94 ctg cat ctg cac tgg ggg gct gca ggt cgt ccg ggc tcg gag cac act 720
95 Leu His Leu His Trp Gly Ala Ala Gly Arg Pro Gly Ser Glu His Thr
96 225      230      235      240
98 gtg gaa ggc cac cgt ttc cct gcc gag atc cac gtg gtt cac ctc agc 768
99 Val Glu Gly His Arg Phe Pro Ala Glu Ile His Val Val His Leu Ser
100      245      250      255
102 acc gcc ttt gcc aga gtt gac gag gcc ttg ggg cgc ccg gga ggc ctg 816
103 Thr Ala Phe Ala Arg Val Asp Glu Ala Leu Gly Arg Pro Gly Gly Leu
104      260      265      270
106 gcc gtg ttg gcc gcc ttt ctg gag gag ggc ccg gaa gaa aac agt gcc 864
107 Ala Val Leu Ala Ala Phe Leu Glu Glu Gly Pro Glu Glu Asn Ser Ala
108      275      280      285
110 tat gag cag ttg ctg tct cgc ttg gaa gaa atc gct gag gaa ggc tca 912
111 Tyr Glu Gln Leu Leu Ser Arg Leu Glu Glu Ile Ala Glu Glu Gly Ser
112      290      295      300
114 gag act cag gtc cca gga ctg gac ata tct gca ctc ctg ccc tct gac 960
115 Glu Thr Gln Val Pro Gly Leu Asp Ile Ser Ala Leu Leu Pro Ser Asp
116 305      310      315      320
118 ttc agc cgc tac ttc caa tat gag ggg tct ctg act aca ccg ccc tgt 1008
119 Phe Ser Arg Tyr Phe Gln Tyr Glu Gly Ser Leu Thr Thr Pro Pro Cys
120      325      330      335
123 gcc cag ggt gtc atc tgg act gtg ttt aac cag aca gtg atg ctg agt 1056
124 Ala Gln Gly Val Ile Trp Thr Val Phe Asn Gln Thr Val Met Leu Ser
125      340      345      350
127 gct aag cag ctc cac acc ctc tct gac acc ctg tgg gga cct ggt gac 1104
128 Ala Lys Gln Leu His Thr Leu Ser Asp Thr Leu Trp Gly Pro Gly Asp

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```

129          355          360          365
131 tct cgg cta cag ctg aac ttc cga gcg acg cag cct ttg aat ggg cga 1152
132 Ser Arg Leu Gln Leu Asn Phe Arg Ala Thr Gln Pro Leu Asn Gly Arg
133          370          375          380
135 gtg att gag gcc tcc ttc cct gct gga gtg gac agc agt cct cgg gct 1200
136 Val Ile Glu Ala Ser Phe Pro Ala Gly Val Asp Ser Ser Pro Arg Ala
137 385          390          395          400
139 gct gag cca gtc cag ctg aat tcc tgc ctg gct gct ggt gac atc cta 1248
140 Ala Glu Pro Val Gln Leu Asn Ser Cys Leu Ala Ala Gly Asp Ile Leu
141          405          410          415
143 gcc ctg gtt ttt ggc ctc ctt ttt gct gtc acc agc gtc gcg ttc ctt 1296
144 Ala Leu Val Phe Gly Leu Leu Phe Ala Val Thr Ser Val Ala Phe Leu
145          420          425          430
147 gtg cag atg aga agg cag cac aga agg gga acc aaa ggg ggt gtg agc 1344
148 Val Gln Met Arg Arg Gln His Arg Arg Gly Thr Lys Gly Gly Val Ser
149          435          440          445
151 tac cgc cca gca gag gta gcc gag act gga gcc tag 1380
152 Tyr Arg Pro Ala Glu Val Ala Glu Thr Gly Ala *
153          450          455
156 <210> SEQ ID NO: 2
157 <211> LENGTH: 459
158 <212> TYPE: PRT
159 <213> ORGANISM: Homo sapiens
161 <400> SEQUENCE: 2
162 Met Ala Pro Leu Cys Pro Ser Pro Trp Leu Pro Leu Leu Ile Pro Ala
163 1          5          10          15
164 Pro Ala Pro Gly Leu Thr Val Gln Leu Leu Leu Ser Leu Leu Leu Leu
165          20          25          30
166 Met Pro Val His Pro Gln Arg Leu Pro Arg Met Gln Glu Asp Ser Pro
167          35          40          45
168 Leu Gly Gly Gly Ser Ser Gly Glu Asp Asp Pro Leu Gly Glu Glu Asp
169          50          55          60
170 Leu Pro Ser Glu Glu Asp Ser Pro Arg Glu Glu Asp Pro Pro Gly Glu
171 65          70          75          80
172 Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro
173          85          90          95
174 Glu Val Lys Pro Lys Ser Glu Glu Glu Gly Ser Leu Lys Leu Glu Asp
175          100          105          110
176 Leu Pro Thr Val Glu Ala Pro Gly Asp Pro Gln Glu Pro Gln Asn Asn
177          115          120          125
178 Ala His Arg Asp Lys Glu Gly Asp Asp Gln Ser His Trp Arg Tyr Gly
179          130          135          140
180 Gly Asp Pro Pro Trp Pro Arg Val Ser Pro Ala Cys Ala Gly Arg Phe
181 145          150          155          160
182 Gln Ser Pro Val Asp Ile Arg Pro Gln Leu Ala Ala Phe Cys Pro Ala
183          165          170          175
184 Leu Arg Pro Leu Glu Leu Leu Gly Phe Gln Leu Pro Pro Leu Pro Glu
185          180          185          190
186 Leu Arg Leu Arg Asn Asn Gly His Ser Val Gln Leu Thr Leu Pro Pro

```

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```

187          195          200          205
188 Gly Leu Glu Met Ala Leu Gly Pro Gly Arg Glu Tyr Arg Ala Leu Gln
189          210          215          220
190 Leu His Leu His Trp Gly Ala Ala Gly Arg Pro Gly Ser Glu His Thr
191 225          230          235          240
192 Val Glu Gly His Arg Phe Pro Ala Glu Ile His Val Val His Leu Ser
193          245          250          255
194 Thr Ala Phe Ala Arg Val Asp Glu Ala Leu Gly Arg Pro Gly Gly Leu
195          260          265          270
196 Ala Val Leu Ala Ala Phe Leu Glu Glu Gly Pro Glu Glu Asn Ser Ala
197          275          280          285
198 Tyr Glu Gln Leu Leu Ser Arg Leu Glu Glu Ile Ala Glu Glu Gly Ser
199          290          295          300
200 Glu Thr Gln Val Pro Gly Leu Asp Ile Ser Ala Leu Leu Pro Ser Asp
201 305          310          315          320
202 Phe Ser Arg Tyr Phe Gln Tyr Glu Gly Ser Leu Thr Thr Pro Pro Cys
203          325          330          335
204 Ala Gln Gly Val Ile Trp Thr Val Phe Asn Gln Thr Val Met Leu Ser
205          340          345          350
206 Ala Lys Gln Leu His Thr Leu Ser Asp Thr Leu Trp Gly Pro Gly Asp
207          355          360          365
208 Ser Arg Leu Gln Leu Asn Phe Arg Ala Thr Gln Pro Leu Asn Gly Arg
209          370          375          380
210 Val Ile Glu Ala Ser Phe Pro Ala Gly Val Asp Ser Ser Pro Arg Ala
211 385          390          395          400
212 Ala Glu Pro Val Gln Leu Asn Ser Cys Leu Ala Ala Gly Asp Ile Leu
213          405          410          415
214 Ala Leu Val Phe Gly Leu Leu Phe Ala Val Thr Ser Val Ala Phe Leu
215          420          425          430
216 Val Gln Met Arg Arg Gln His Arg Arg Gly Thr Lys Gly Gly Val Ser
217          435          440          445
218 Tyr Arg Pro Ala Glu Val Ala Glu Thr Gly Ala
219          450          455
222 <210> SEQ ID NO: 3
223 <211> LENGTH: 540
224 <212> TYPE: DNA
225 <213> ORGANISM: Artificial Sequence
227 <220> FEATURE:
228 <223> OTHER INFORMATION: Coding sequence for human CA IX proteoglycan
229 domain construct
W--> 231 <221> NAME/KEY: CDS
232 <222> LOCATION: (1)...(540)
W--> 237 <400> 3
238 atg gct ccc ctg tgc ccc agc ccc tgg ctc cct ctg ttg atc ccg gcc 48
239 Met Ala Pro Leu Cys Pro Ser Pro Trp Leu Pro Leu Leu Ile Pro Ala
240 1 5 10 15
242 ctt gct cca ggc ctc act gtg caa ctg ctg ctg tca ctg ctg ctt ctg 96
243 Leu Ala Pro Gly Leu Thr Val Gln Leu Leu Leu Ser Leu Leu Leu
244 20 25 30

```

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Output Set: N:\CRF4\03082007\J525535.raw

```

246 atg cct gtc cat ccc cag agg ttg ccc cgg atg cag gag gat tcc ccc 144
247 Met Pro Val His Pro Gln Arg Leu Pro Arg Met Gln Glu Asp Ser Pro
248      35      40      45
250 ttg gga gga ggc tct tct ggg gaa gat gac cca ctg ggc gag gag gat 192
251 Leu Gly Gly Gly Ser Ser Gly Glu Asp Asp Pro Leu Gly Glu Glu Asp
252      50      55      60
254 ctg ccc agt gaa gag gat tca ccc aga gag gag gat cca ccc gga gag 240
255 Leu Pro Ser Glu Glu Asp Ser Pro Arg Glu Glu Asp Pro Pro Gly Glu
256 65      70      75      80
258 gag gat cta cct gga gag gag gat cta cct gga gag gag gat cta cct 288
259 Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro
260      85      90      95
262 gaa gtt aag cct aaa tca gaa gaa gag ggc tcc ctg aag tta gag gat 336
263 Glu Val Lys Pro Lys Ser Glu Glu Gly Ser Leu Lys Leu Glu Asp
264      100      105      110
266 cta cct act gtt gag gct cct gga gat cct caa gaa ccc cag aat aat 384
267 Leu Pro Thr Val Glu Ala Pro Gly Asp Pro Gln Glu Pro Gln Asn Asn
268      115      120      125
270 gcc cat agg agc tcg agc atc cta gcc ctg gtt ttt ggc ctc ctt ttt 432
271 Ala His Arg Ser Ser Ser Ile Leu Ala Leu Val Phe Gly Leu Leu Phe
272      130      135      140
274 gct gtc acc agc gtc gcg ttc ctt gtg cag atg aga agg cag cac aga 480
275 Ala Val Thr Ser Val Ala Phe Leu Val Gln Met Arg Arg Gln His Arg
276 145      150      155      160
278 agg gga acc aaa ggg ggt gtg agc tac cgc cca gca gag gta gcc gag 528
279 Arg Gly Thr Lys Gly Gly Val Ser Tyr Arg Pro Ala Glu Val Ala Glu
280      165      170      175
282 act gga gcc tag 540
283 Thr Gly Ala *
287 <210> SEQ ID NO: 4
288 <211> LENGTH: 179
289 <212> TYPE: PRT
C--> 290 <213> ORGANISM: Artificial Sequence
292 <220> FEATURE:
294 <223> OTHER INFORMATION: Polypeptide encoded by coding sequence for human
295      CA IX proteoglycan domain construct
297 <400> SEQUENCE: 4
298 Met Ala Pro Leu Cys Pro Ser Pro Trp Leu Pro Leu Leu Ile Pro Ala
299 1      5      10      15
300 Leu Ala Pro Gly Leu Thr Val Gln Leu Leu Leu Ser Leu Leu Leu Leu
301      20      25      30
302 Met Pro Val His Pro Gln Arg Leu Pro Arg Met Gln Glu Asp Ser Pro
303      35      40      45
304 Leu Gly Gly Gly Ser Ser Gly Glu Asp Asp Pro Leu Gly Glu Glu Asp
305      50      55      60
306 Leu Pro Ser Glu Glu Asp Ser Pro Arg Glu Glu Asp Pro Pro Gly Glu
307 65      70      75      80
308 Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro
309      85      90      95

```

VERIFICATION SUMMARY

DATE: 03/08/2007

PATENT APPLICATION: US/10/525,535

TIME: 14:57:11

Input Set : N:\efs\03_08_07\10525535_efs\324503SequenceListing.txt

Output Set: N:\CRF4\03082007\J525535.raw

L:231 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:237 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:290 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:4
L:333 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:336 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:5
L:500 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:503 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7
L:657 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:660 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:9